FastQC Report

Summary

✅ [Basic Statistics](#)

✅ [Per base sequence quality](#)

⚠️ [Per tile sequence quality](#)
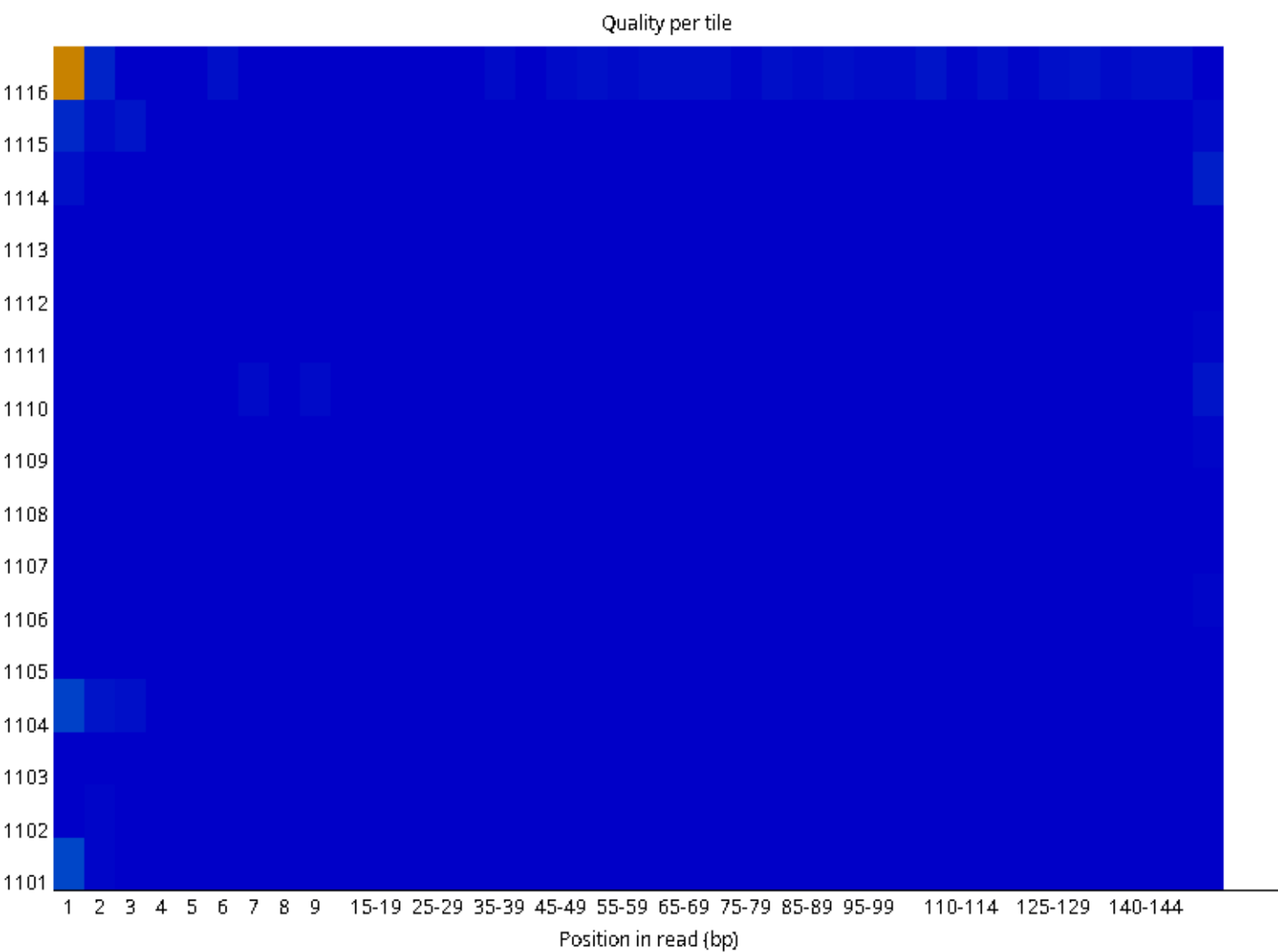
✅ [Per sequence quality scores](#)

⚠️ [Per base sequence content](#)
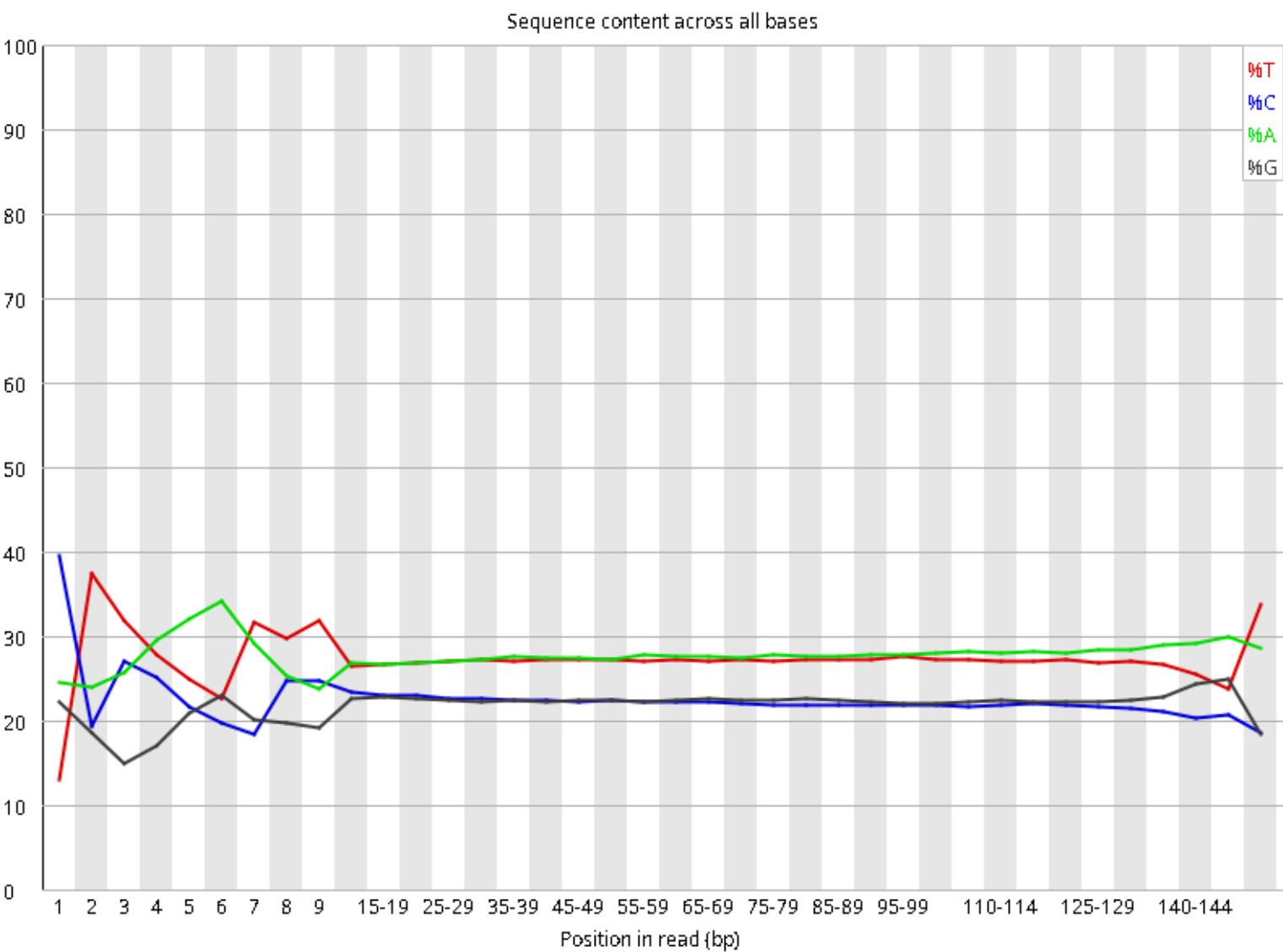
❌ [Per sequence GC content](#)
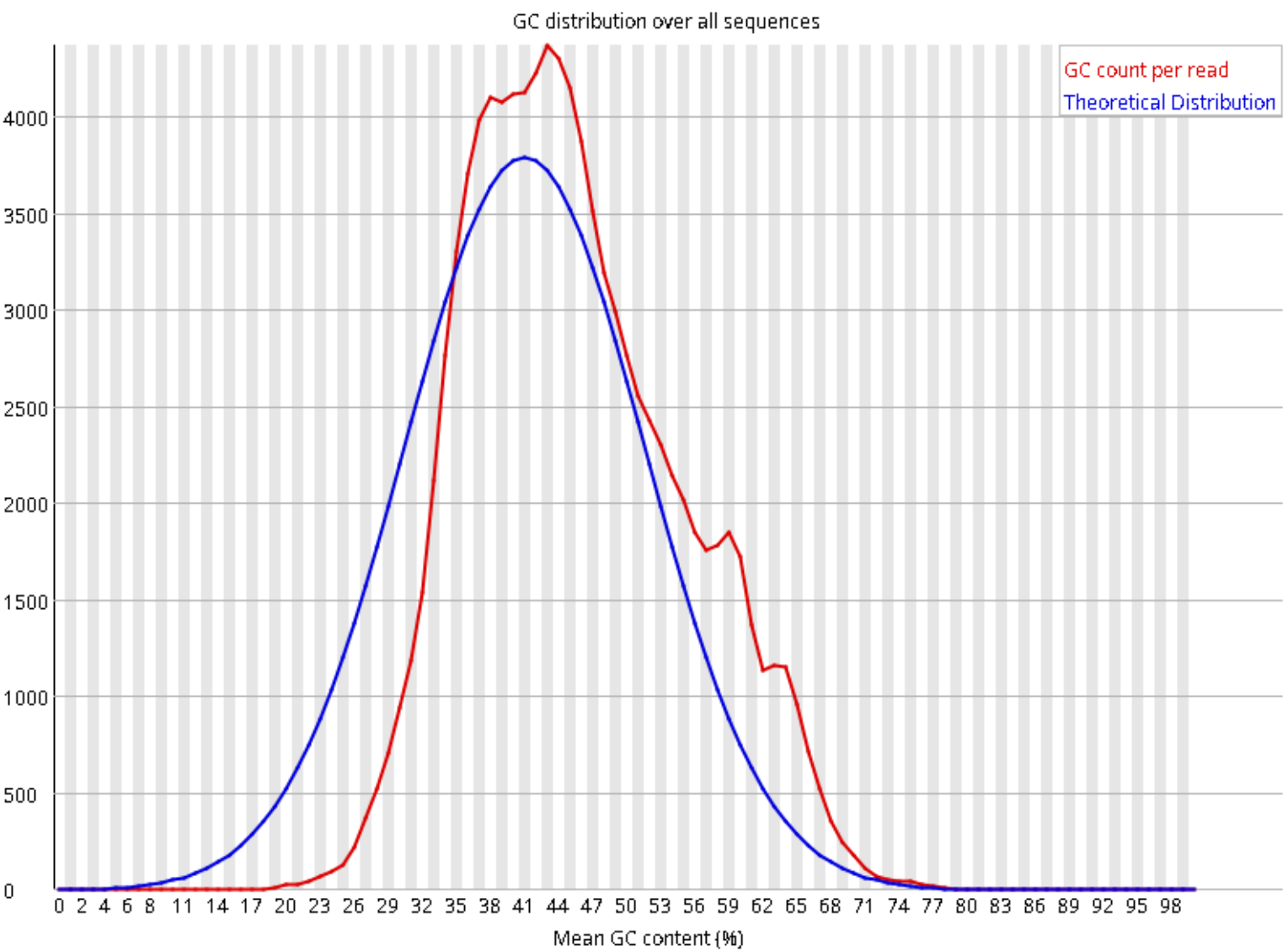
✅ [Per base N content](#)
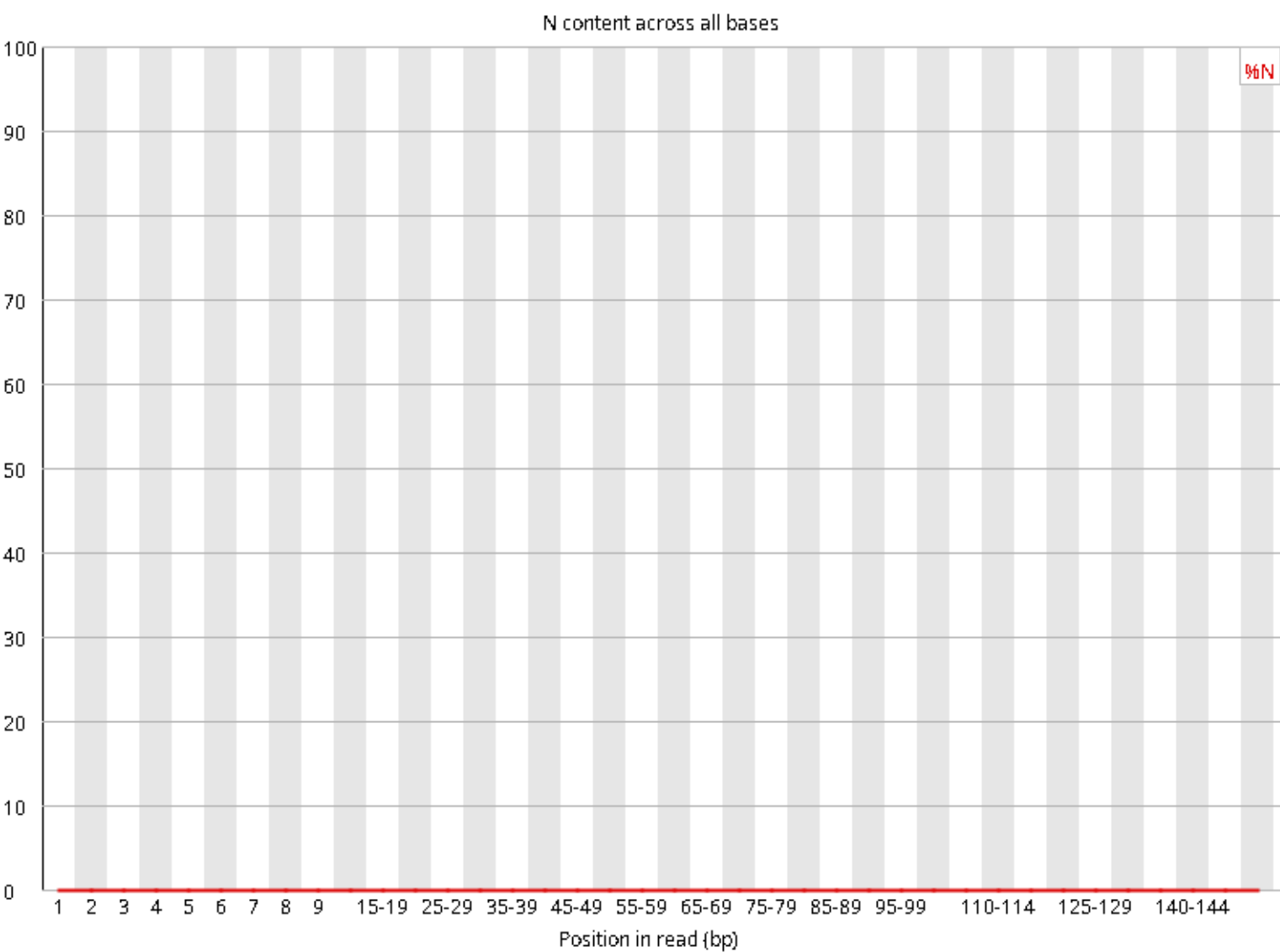
⚠️ [Sequence Length Distribution](#)
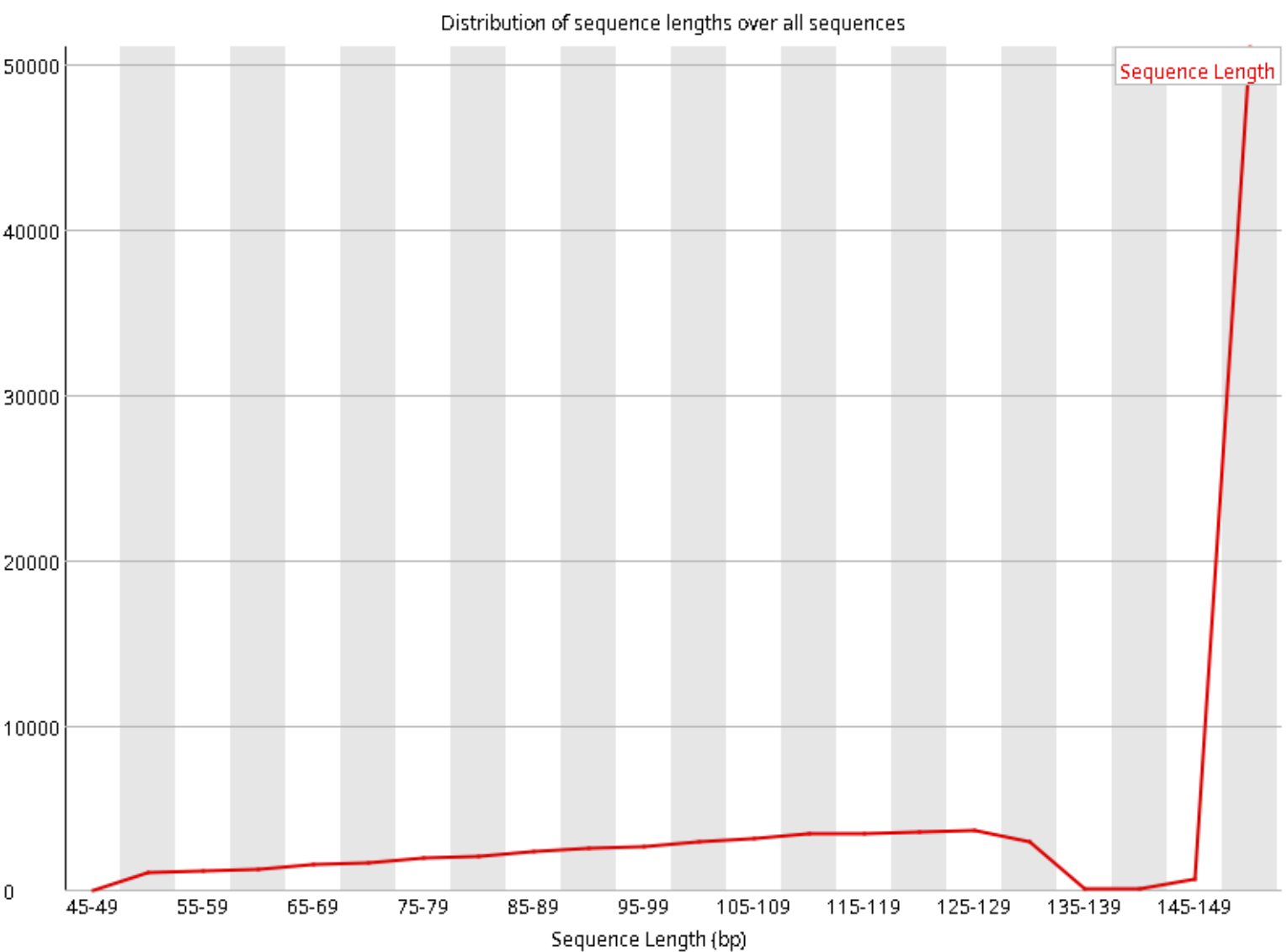
⚠️ [Sequence Duplication Levels](#)

✅ [Overrepresented sequences](#)

✅ [Adapter Content](#)

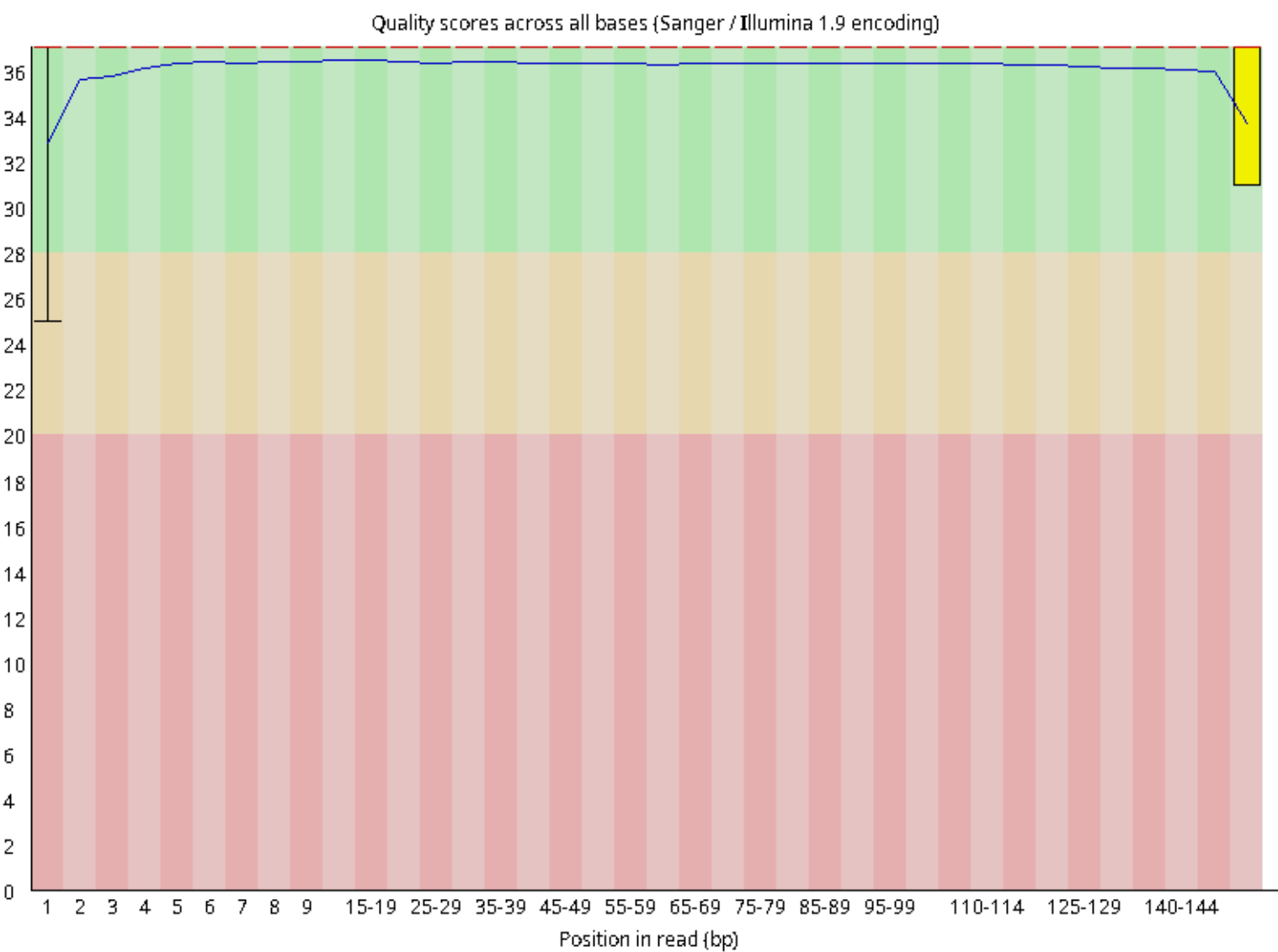## ✅ Basic Statistics

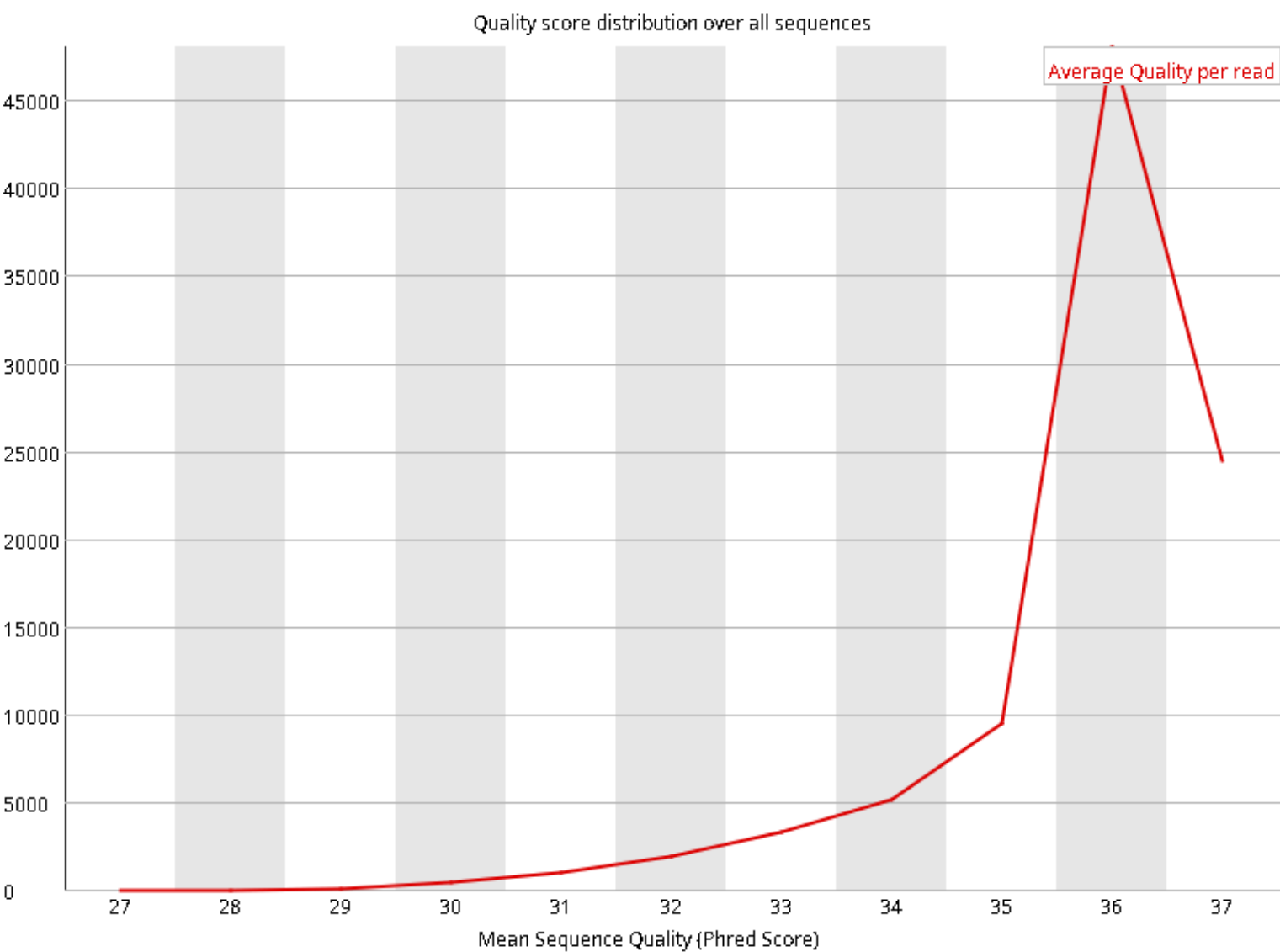| Measure	Value
Filename	SRR33784444_1_paired.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	94421
Sequences flagged as poor quality	0
Sequence length	50-151
%GC	44

✅ Per base sequence quality

Quality scores across all bases (Sanger / Illumina 1.9 encoding)

Per tile sequence quality

Quality per tile

Position in read (bp)

✅ Per sequence quality scores

Quality score distribution over all sequences

Average Quality per read

Mean Sequence Quality (Phred Score)

Per base sequence content

Sequence content across all bases

Per sequence GC content

GC distribution over all sequences

Per base N content

N content across all bases

Sequence Length Distribution

Distribution of sequence lengths over all sequences

Sequence Duplication Levels

Percent of seqs remaining if deduplicated 69.82%

Overrepresented sequences

No overrepresented sequences

Adapter Content